

SEQUENCE LISTING

<110> Butcher, Eugene C.  
 Campbell, James J.  
 Rottman, James B.  
 Wu, Lijan

<120> Modulation of Systemic Memory T Cell  
 Trafficking

<130> STAN-110CON

<140> Unassigned  
 <141> 2001-04-17

<150> 09/232,878  
 <151> 1999-01-15

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1  
 <211> 1677  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> CDS  
 <222> (183)...(1265)  
 <223> CCR4, Chemokine receptor coding sequence

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tctctcattt cccttctcct tctccctcag tctccacatt caacattgac aagtccattc	180
agaaaagcaa gctgcttctg gttgggcca gacgtgcctt gaggagcctg tagagttaaa	227
aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata	
Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile	
1 5 10 15	
tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa	275
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys	
20 25 30	
gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc	323
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser	
35 40 45	
ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc	371
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val	
50 55 60	
ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc	419
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu	
65 70 75	
aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg	467

Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp	95	
80 85	90	
ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag	515	
Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys		
100 105 110		
atg att tcc tgg atg tac ttg gtc ttt tac agt ggc ata ttc ttt	563	
Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe		
115 120 125		
gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg	611	
Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val		
130 135 140		
ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg	659	
Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu		
145 150 155		
gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc	707	
Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe		
160 165 170 175		
agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac	755	
Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr		
180 185 190		
tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac	803	
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn		
195 200 205		
att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc	851	
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser		
210 215 220		
atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag	899	
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys		
225 230 235		
gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg	947	
Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp		
240 245 250 255		
aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa	995	
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu		
260 265 270		
gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag	1043	
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln		
275 280 285		
gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc	1091	
Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile		
290 295 300		
tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc	1139	
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe		
305 310 315		

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc	1187
Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu	
320 325 330 335	
caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc	1235
Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr	
340 345 350	
atg gat cat gat ctt cat gat gct ctg tag gaaaaatgaa atggtaaat	1285
Met Asp His Asp Leu His Asp Ala Leu *	
355 360	
gcagagtcaa tgaactttc cacattcaga gcttacttta aaattggtat ttttaggtaa	1345
gagatccctg agccagtgtc aggaggaagg cttacaccca cagtggaaag acagcttc	1405
atcctgcagg cagcttttc tctccacta gacaagtcca gcctggcaag gttcacctg	1465
ggctgaggca tccttcctca caccaggcgt gcctgcaggc atgagtcaat ctgatgagaa	1525
ctctgaggcag tgcttgaatg aagttgttagg taatattgca aggcaaagac tattcccttc	1585
taacctgaac tgatggttt ctccagaggg aattgcagag tactggctga tggagtaaat	1645
cgctacctt tgctgtggca aatggggcccc cg	1677
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<212> PRT	
<213> H. sapiens	
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Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu	
20 25 30	
Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu	
35 40 45	
Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu	
50 55 60	
Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn	
65 70 75 80	
Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly	
85 90 95	
Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met	
100 105 110	
Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val	
115 120 125	
Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe	
130 135 140	
Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala	
145 150 155 160	
Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser	
165 170 175	
Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser	
180 185 190	
Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile	
195 200 205	
Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met	
210 215 220	
Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala	
225 230 235 240	
Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr	

245	250	255	
Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val			
260	265	270	
Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala			
275	280	285	
Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr			
290	295	300	
Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys			
305	310	315	320
Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln			
325	330	335	
Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met			
340	345	350	
Asp His Asp Leu His Asp Ala Leu			
355	360		

<210> 3  
 <211> 538  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> CDS  
 <222> (53)...(337)  
 <223> Coding sequence for TARC chemokine

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Met Ala	
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cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg	106
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu	
5 10 15	
cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc	154
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys	
20 25 30	
ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg	202
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp	
35 40 45 50	
tac cag aca tct gag gac tcc agg gat gcc atc gtt ttt gta act	250
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr	
55 60 65	
gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aga gtg aag	298
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys	
70 75 80	
aat gca gtt aaa tac ctg caa agc ctt gag agg tct tga agcctcctca	347
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser *	
85 90	
ccccagactc ctgactgtct cccgggacta cctgggacct ccaccgttgg tggtcaccgc	407
ccccacccctg agccgcctgg tccagggag gccttccagg gacgaagaag agccacagtg	467
agggagatcc catcccccttg tctgaactgg agccatgggc acaaagggcc cagattaaag	527

tctttatcct c

<210> 4  
 <211> 94  
 <212> PRT  
 <213> H. sapiens

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 Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala  
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 5 10  
 Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu  
 20 25 30  
 Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys  
 35 40 45  
 Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe  
 50 55 60  
 Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg  
 65 70 75 80  
 Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser  
 85 90

<210> 5  
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 <212> DNA  
 <213> H. sapiens

<220>  
 <221> CDS  
 <222> (20)...(301)  
 <223> Coding sequence for MDC chemokine

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 52  
 Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val  
 1 5 10

ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac  
 100  
 Leu Val Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr  
 15 20 25

ggc gcc aac atg gaa gac agc gtc tgc cgt gat tac gtc cgt tac  
 148  
 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr  
 30 35 40

cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc  
 196  
 Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser  
 45 50 55

tgc ccg agg cct ggc gtg gtg cta acc ttc agg gat aag gag atc  
 244  
 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile  
 60 65 70 75

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg  
 292  
 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu  
 80 85 90

agc caa tga agagcctact ctgatgaccg tggccttggc tcctccagga  
 Ser Gln \*

341

aggctcgat	gcctcaccc	cctgcccatt	tagctgctcc	ccggccagaag	cctgtgccaa	401
ctctctgcat	tcctctgatct	ccatccctgt	ggctgtcacc	cttggtcacc	tccgtctgt	461
cactgcccac	tccccccctga	ccccctctaacc	ccatccctgt	cctccctccc	tgcagtcaga	521
gggtcctgtt	cccatcagcg	atccccctgc	ttaaaccctt	ccatgactcc	ccactgcct	581
aagctgaggt	cagtctccca	agcctggcat	gtggccctct	ggatctgggt	tccatctctg	641
tctccagcct	gcccacttcc	cttcatgaat	gttgggttct	agctccctgt	tctccaaacc	701
catactacac	atcccacttc	tgggtcttt	cctgggatgt	tgctgacact	cagaaaagtcc	761
caccacccctgc	acatgtgtag	ccccaccaggc	cctccaaggc	attgctcgcc	caaggcgtg	821
gttaattccat	ttcatgtatt	agatgtcccc	tggccctctg	tcccctctta	ataaccctag	881
tcacagtc	cgcagattct	tgggatttgg	ggggtttctc	ccccacccct	ccactagttg	941
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gaatcaactgc	gcctggctt	cttccctct	tgagaaat	tctttcata	cagcaagtat	2501
gggacagcag	tgtcccagg	aaaggacata	atgttacaa	gtgtctggc	cttctgagg	2561
gaggctgggt	ccgctctgca	gggtatttga	acctgtggaa	ttggaggagg	ccatttact	2621
ccctgaaccc	agcctgacaa	atcacagtga	gaatgttac	cttataaggct	tgctgtgggg	2681
ctcagggttga	aaagtgtggg	agtgacactg	cctaggcatc	cagctcgt	tcatccagg	2741
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tgcctactgc	ccatgaaacgg	ggccctcaag	cgtcctggga	tctccttctc	cctcctgtcc	2861
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aa						2923

<210> 6  
<211> 93  
<212> PRT  
<213> *H. sapiens*

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly  
50 55 60  
Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg  
65 70 75 80  
Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln  
85 90